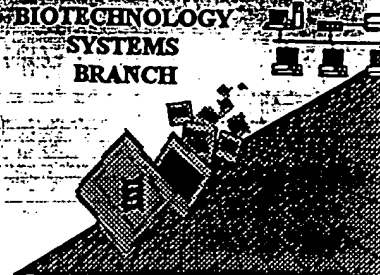# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/150 947 A_

Art Unit / Team No. : _1645_

Date Processed by STIC: _6 - 8 - 00_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/150,947A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                               This may occur if your file was retrieved in a word processor after creating it.
                               Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                               This may occur if your file was retrieved in a word processor after creating it.
                               Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                               Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                               As per the rules, each n or Xaa can only represent a single residue.
                               Please present the maximum number of each residue having variable length and
                               indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                               sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                               to the subsequent amino acid sequence.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                               (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                               This sequence is intentionally skipped

                               Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                               <400> sequence id number
                               000

10 ✓ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" _
                               Please explain source of genetic material in <220> to <223> section.
                               (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted**
                               file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                               Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

1645

```
              RAW SEQUENCE LISTING              DATE: 06/08/2000
              PATENT APPLICATION:  US/09/150,947A    TIME: 08:04:01

              Input Set : A:\A31967-PCT-USA seq list.txt
              Output Set: N:\CRF3\06082000\I150947A.raw
```

P.P. 2, 3

```
 4 <110> APPLICANT: Raymond Kaempfer
 5        Gala Arad
 7 <120> TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
 8        ANTAGONISTS AND VACCINES
11 <130> FILE REFERENCE: A31967-PCT-USA-A
13 <140> CURRENT APPLICATION NUMBER: 09/150,947A
14 <141> CURRENT FILING DATE: 1998-09-10
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 26
22 <212> TYPE: PRT
23 <213> ORGANISM: Staphylococcal aureus
25 <400> SEQUENCE: 1
26  Ser Glu Gln Glu Asn Cys Glu Leu Ile Ser Thr Ile Asn Gly Thr Asn
27   1               5               10              15
28  Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
29           20                  25
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 12
33 <212> TYPE: PRT
34 <213> ORGANISM: Staphylococcal aureus
36 <400> SEQUENCE: 2
37  Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
38   1               5               10
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 10
42 <212> TYPE: PRT
43 <213> ORGANISM: Staphylococcal aureus
45 <220> FEATURE:
46 <221> NAME/KEY: VARIANT
47 <222> LOCATION: (0)...(0)
49 <400> SEQUENCE: 3
50  Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
51   1               5                   10
53 <210> SEQ ID NO: 4
54 <211> LENGTH: 10
55 <212> TYPE: PRT
56 <213> ORGANISM: Staphylococcal aureus
58 <400> SEQUENCE: 4
59  Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
60   1               5                   10
62 <210> SEQ ID NO: 5
63 <211> LENGTH: 13
64 <212> TYPE: PRT
65 <213> ORGANISM: Staphylococcal aureus
67 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A   TIME: 08:04:01

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
 68 <223> OTHER INFORMATION: n-lauryl cysteine residue
 70 <400> SEQUENCE: 5
 71  Xaa Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
 72  1               5                   10
 74 <210> SEQ ID NO: 6
 75 <211> LENGTH: 13
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Staphylococcal aureus
 79 <220> FEATURE:
 80 <223> OTHER INFORMATION: n-lauryl cysteine
 82 <400> SEQUENCE: 6
 83  Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
 84  1               5                   10
 86 <210> SEQ ID NO: 7
 87 <211> LENGTH: 16
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Staphylococcal aureus
 91 <400> SEQUENCE: 7
 92  Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
 93  1               5                   10                  15
 95 <210> SEQ ID NO: 8
 96 <211> LENGTH: 35
 97 <212> TYPE: PRT
 98 <213> ORGANISM: Staphylococcal aureus
100 <400> SEQUENCE: 8
101  Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
102  1               5                   10                  15
103  Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys Lys Ala Thr Val
104              20                  25                  30
105  Glu Leu Asp
106              35
108 <210> SEQ ID NO: 9
109 <211> LENGTH: 14
110 <212> TYPE: PRT
111 <213> ORGANISM: Staphylococcal aureus
113 <220> FEATURE:
114 <221> NAME/KEY: DISULFID
115 <222> LOCATION: (1)...(1)
117 <221> NAME/KEY: DISULFID
118 <222> LOCATION: (14)...(14)
120 <221> NAME/KEY: DISULFID
121 <222> LOCATION: (14)...(14)
123 <400> SEQUENCE: 9
124  Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
125  1               5                   10
127 <210> SEQ ID NO: 10
128 <211> LENGTH: 14
129 <212> TYPE: PRT
130 <213> ORGANISM: Staphylococcal aureus
```

Handwritten annotations:

No <222>: numerical location of Xaa's within Sequence. See Error Summary Sheet, #10

delete "c"

These describe bonds, but no explanation of what Xaa's represent. Xaa can only represent a single amino acid, nothing else

duplicated - see above

RAW SEQUENCE LISTING   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A   TIME: 08:04:01

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
132 <220> FEATURE:
133 <223> OTHER INFORMATION: D-alanine residue
135 <223> OTHER INFORMATION: D-alanine residue
137 <400> SEQUENCE: 10
138 Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
139     1           5               10
141 <210> SEQ ID NO: 11
142 <211> LENGTH: 14
143 <212> TYPE: PRT
144 <213> ORGANISM: Staphylococcal aureus
146 <220> FEATURE:
147 <223> OTHER INFORMATION: N-acetyl group
149 <223> OTHER INFORMATION: D-alanine residue
151 <400> SEQUENCE: 11
152 Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
153     1           5               10
155 <210> SEQ ID NO: 12
156 <211> LENGTH: 239
157 <212> TYPE: PRT
158 <213> ORGANISM: Staphylococcal aureus
160 <400> SEQUENCE: 12
161 Glu Ser Gln Pro Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys
162     1           5               10              15
163 Phe Thr Gly Leu Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His
164             20              25              30
165 Val Ser Ala Ile Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp
166         35              40              45
167 Leu Ile Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val
168         50              55              60
169 Arg Val Glu Phe Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys
170 65              70               75              80
171 Tyr Val Asp Val Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser
172             85              90              95
173 Lys Lys Thr Asn Asp Ile Asn Ser His Glu Thr Asp Lys Arg Lys Thr
174             100             105             110
175 Cys Met Tyr Gly Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys
176         115             120             125
177 Tyr Arg Ser Ile Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu
178         130             135             140
179 Ser Phe Asp Val Gln Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu
180 145             150             155             160
181 Asp Tyr Leu Thr Arg His Tyr Leu Val Lys Asn Lys Lys Leu Tyr Glu
182             165             170             175
183 Phe Asn Asn Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn
184             180             185             190
185 Glu Asn Ser Phe Trp Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe
186         195             200             205
187 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Met Val Asp
188         210             215             220
```

```
189  Ser Lys Asp Val Lys Ile Glu Val Tyr Leu Thr Thr Lys Lys Lys
190  225             230             235
```

VERIFICATION SUMMARY   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A   TIME: 08:04:02

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
L:71  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:71  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:71  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:83  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:83  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:83  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:124 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:124 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:138 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:152 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:152 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:152 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
```